

# SEQUENCE LISTING

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 Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser  
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Gln Val Pro Ser Ala Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys	
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<213> *Perilla frutescens*

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 Arg Gly Ser Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn Asp Asp Val  
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 Arg Leu Ser His Val Pro Thr Ala Leu Leu Trp Val Glu Pro Ala Thr  
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 Val Leu Cys Ile Tyr His Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile  
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 Ala Trp Arg Arg Met Ser Arg Thr Ala Ala Gly Ser Asn Gly Leu Ile  
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Glu Glu Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu Glu Pro	
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 Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr  
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Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys Trp	
100 105 110	
aca atc gtg tgg tcc atc atc ttt aca tgg atg ttc cta ggc aca aaa	683
Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr Lys	
115 120 125 130	
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Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly Leu	
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Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser Asn	
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Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe Thr	
165 170 175	
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Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg Ile	
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Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe Leu	
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Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile Arg	
260 265 270	

aca ttc ata tac aac cag gag gtt gat tgg tta tac tat ttg gcc ttt 1163  
 Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala Phe  
 275 280 285 290  
 tgt ctc gtt gtt gtt gga ata ttc ata tat aca aaa aca gag aag gat 1211  
 Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys Asp  
 295 300 305  
 cct aac aat acg aga gcc ctt gag aat gga aac ttg gat cat gaa tat 1259  
 Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu Tyr  
 310 315 320  
 agt ctc ctt gag gat caa gat gac aca cca aga aaa cca tagctagctt 1308  
 Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro  
 325 330 335  
 tgcccacaat cttttcatca acagtttttaa ataattcgtg agggggagag agatcgagat 1368  
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 aacagctatg accatgatta cgccaagctc gaaattaacc ctactaaag ggaacaaaag 180  
 ctggagctcc acgcggtggc ggccgctcta gaactagtgg atccccggg ctgcaggaat 240  
 tccgttgctg tcgccacaat ttacaaacca agaaattaag catcccttcc ccccccttaa 300  
 aaaacataca agtttttaat ttttactaa gcaagaaaat atg gtg cag cct cat gtc 358  
 Met Val Gln Pro His Val  
 1 5  
 atc tta aca aca ttt cca gca caa ggc cat att aat cca gca ctt caa 406  
 Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln  
 10 15 20  
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 Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr  
 25 30 35  
 agc att tat gcc caa agc cgt atg gat gaa aaa tcc att ctt aat gca 502  
 Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala  
 40 45 50

cca	aaa	gga	ttg	aat	ttc	att	cca	ttt	tcc	gat	ggc	ttt	gat	gaa	ggc	550
Pro	Lys	Gly	Leu	Asn	Phe	Ile	Pro	Phe	Ser	Asp	Gly	Phe	Asp	Glu	Gly	
55					60					65					70	
ttt	gat	cat	tca	aaa	gac	cct	gta	ttt	tac	atg	tca	caa	ctt	cgt	aaa	598
Phe	Asp	His	Ser	Lys	Asp	Pro	Val	Phe	Tyr	Met	Ser	Gln	Leu	Arg	Lys	
				75					80					85		
tgt	gga	agt	gaa	act	gtc	aaa	aaa	ata	att	ctc	act	tgc	tct	gaa	aat	646
Cys	Gly	Ser	Glu	Thr	Val	Lys	Lys	Ile	Ile	Leu	Thr	Cys	Ser	Glu	Asn	
			90					95				100				
gga	cag	cct	ata	act	tgc	cta	ctt	tac	tcc	att	ttc	ctt	cct	tgg	gca	694
Gly	Gln	Pro	Ile	Thr	Cys	Leu	Leu	Tyr	Ser	Ile	Phe	Leu	Pro	Trp	Ala	
	105						110				115					
gca	gag	gta	gca	cgt	gaa	gtt	cac	atc	cct	tct	gct	ctt	ctt	tgg	agt	742
Ala	Glu	Val	Ala	Arg	Glu	Val	His	Ile	Pro	Ser	Ala	Leu	Leu	Trp	Ser	
	120					125				130						
caa	cca	gca	aca	ata	ttg	gac	ata	tat	tac	ttc	aac	ttt	cat	gga	tat	790
Gln	Pro	Ala	Thr	Ile	Leu	Asp	Ile	Tyr	Tyr	Phe	Asn	Phe	His	Gly	Tyr	
135				140				145					150			
gaa	aaa	gct	atg	gct	aat	gaa	tcc	aat	gat	cca	aat	tgg	tcc	att	caa	838
Glu	Lys	Ala	Met	Ala	Asn	Glu	Ser	Asn	Asp	Pro	Asn	Trp	Ser	Ile	Gln	
			155					160				165				
ctt	ccc	ggg	ctt	cca	cta	ctg	gaa	act	cga	gat	ctt	cct	tca	ttt	tta	886
Leu	Pro	Gly	Leu	Pro	Leu	Leu	Glu	Thr	Arg	Asp	Leu	Pro	Ser	Phe	Leu	
		170					175				180					
ctt	cct	tat	ggc	gca	aaa	ggg	agt	ctt	cga	gtt	gca	ctt	cca	cca	ttc	934
Leu	Pro	Tyr	Gly	Ala	Lys	Gly	Ser	Leu	Arg	Val	Ala	Leu	Pro	Pro	Phe	
	185					190				195						
aaa	gaa	ttg	ata	gac	aca	tta	gat	gct	gaa	acc	act	cct	aag	att	ctt	982
Lys	Glu	Leu	Ile	Asp	Thr	Leu	Asp	Ala	Glu	Thr	Thr	Pro	Lys	Ile	Leu	
	200					205			210							
gtg	aat	aca	ttt	gat	gaa	tta	gag	cct	gag	gca	ctc	aat	gca	att	gaa	1030
Val	Asn	Thr	Phe	Asp	Glu	Leu	Glu	Pro	Glu	Ala	Leu	Asn	Ala	Ile	Glu	
215				220				225						230		
ggc	tat	aag	ttt	tat	gga	att	gga	ccg	ttg	att	cct	tct	gct	ttc	ttg	1078
Gly	Tyr	Lys	Phe	Tyr	Gly	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu	
			235				240				245					

ggg	gga	aat	gac	cct	tta	gat	gct	tca	ttt	ggg	ggg	gat	ctt	ttt	caa	1126
Gly	Gly	Asn	Asp	Pro	Leu	Asp	Ala	Ser	Phe	Gly	Gly	Asp	Leu	Phe	Gln	
250				255				260								
aat	tca	aat	gac	tat	atg	gaa	tgg	tta	aac	tca	aag	cca	aat	tca	tca	1174
Asn	Ser	Asn	Asp	Tyr	Met	Glu	Trp	Leu	Asn	Ser	Lys	Pro	Asn	Ser	Ser	
265				270				275								
gtt	gtt	tat	ata	tct	ttt	ggg	agt	cta	atg	aat	cca	tct	att	agc	caa	1222
Val	Val	Tyr	Ile	Ser	Phe	Gly	Ser	Leu	Met	Asn	Pro	Ser	Ile	Ser	Gln	
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atg	gag	gag	ata	tca	aaa	ggg	ttg	ata	gac	ata	gga	agg	ccg	ttt	tta	1270
Met	Glu	Glu	Ile	Ser	Lys	Gly	Leu	Ile	Asp	Ile	Gly	Arg	Pro	Phe	Leu	
295				300				305				310				
tgg	gtg	ata	aaa	gaa	aat	gaa	aaa	ggc	aaa	gaa	gaa	gag	aat	aaa	aag	1318
Trp	Val	Ile	Lys	Glu	Asn	Glu	Lys	Gly	Lys	Glu	Glu	Glu	Asn	Lys	Lys	
315				320				325								
ctt	ggg	tgt	att	gaa	gaa	ttg	gaa	aaa	ata	gga	aaa	ata	gtt	cca	tgg	1366
Leu	Gly	Cys	Ile	Glu	Glu	Leu	Glu	Lys	Ile	Gly	Lys	Ile	Val	Pro	Trp	
330				335				340								
tgt	tca	caa	ctt	gaa	gtt	cta	aaa	cat	cca	tct	tta	gga	tgt	ttt	gtt	1414
Cys	Ser	Gln	Leu	Glu	Val	Leu	Lys	His	Pro	Ser	Leu	Gly	Cys	Phe	Val	
345				350				355								
tct	cat	tgt	gga	tgg	aat	tca	gcc	tta	gag	agt	tta	gct	tgt	gga	gtg	1462
Ser	His	Cys	Gly	Trp	Asn	Ser	Ala	Leu	Glu	Ser	Leu	Ala	Cys	Gly	Val	
360				365				370								
cca	gtt	gtg	gca	ttt	cct	caa	tgg	aca	gat	caa	atg	aca	aat	gcc	aaa	1510
Pro	Val	Val	Ala	Phe	Pro	Gln	Trp	Thr	Asp	Gln	Met	Thr	Asn	Ala	Lys	
375				380				385				390				
caa	gtt	gaa	gat	gtg	tgg	aaa	agt	gga	gta	aga	gtg	aga	ata	aat	gaa	1558
Gln	Val	Glu	Asp	Val	Trp	Lys	Ser	Gly	Val	Arg	Val	Arg	Ile	Asn	Glu	
395				400				405								
gat	ggg	gtt	gtt	gaa	agt	gag	gaa	atc	aaa	agg	tgt	att	gaa	ttg	gta	1606
Asp	Gly	Val	Val	Glu	Ser	Glu	Glu	Ile	Lys	Arg	Cys	Ile	Glu	Leu	Val	
410				415				420								
atg	gat	gga	gga	gag	aaa	ggg	gaa	gaa	ttg	aga	aag	aat	gct	aag	aaa	1654
Met	Asp	Gly	Gly	Glu	Lys	Gly	Glu	Glu	Leu	Arg	Lys	Asn	Ala	Lys	Lys	
425				430				435								

tgg aaa gaa ttg gct aga gaa gct gtg aag gaa ggt gga tct tca cac 1702  
 Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His  
 440 445 450  
 aag aat tta aag gct ttt att gat gat gtt gcc aaa ggg ttt taatatttac 1754  
 Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe  
 455 460 465 468  
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<213> *Perilla frutescens*

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 Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu Leu Lys Ala Gly Thr  
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 Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn  
 35 40 45  
 Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala  
 50 55 60  
 Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Cys Gly Asp Gly Lys  
 65 70 75 80  
 Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn  
 85 90 95  
 Leu Leu Leu Asn Asn His Asp Val Thr Phe Val Val Tyr Ser His Leu  
 100 105 110  
 Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser Gln Val Pro Ser Ala  
 115 120 125  
 Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr Tyr Phe Tyr  
 130 135 140

Phe	Asn	Gly	Tyr	Ala	Asp	Glu	Ile	Asp	Ala	Gly	Ser	Asp	Glu	Ile	Gln	145	150	155	160
Leu	Pro	Arg	Leu	Pro	Pro	Leu	Glu	Gln	Arg	Ser	Leu	Pro	Thr	Phe	Leu	165	170	175	
Leu	Pro	Glu	Thr	Pro	Glu	Arg	Phe	Arg	Leu	Met	Met	Lys	Glu	Lys	Leu	180	185	190	
Glu	Thr	Leu	Asp	Gly	Glu	Glu	Lys	Ala	Lys	Val	Leu	Val	Asn	Thr	Phe	195	200	205	
Asp	Ala	Leu	Glu	Pro	Asp	Ala	Leu	Thr	Ala	Ile	Asp	Arg	Tyr	Glu	Leu	210	215	220	
Ile	Gly	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu	Asp	Gly	Gly	Asp	225	230	235	240
Pro	Ser	Glu	Thr	Ser	Tyr	Gly	Gly	Asp	Leu	Phe	Glu	Lys	Ser	Glu	Glu	245	250	255	
Asn	Asn	Cys	Val	Glu	Trp	Leu	Asp	Thr	Lys	Pro	Lys	Ser	Ser	Val	Val	260	265	270	
Tyr	Val	Ser	Phe	Gly	Ser	Val	Leu	Arg	Phe	Pro	Lys	Ala	Gln	Met	Glu	275	280	285	
Glu	Ile	Gly	Lys	Gly	Leu	Leu	Ala	Cys	Gly	Arg	Pro	Phe	Leu	Trp	Met	290	295	300	
Ile	Arg	Glu	Gln	Lys	Asn	Asp	Asp	Gly	Glu	Glu	Glu	Glu	Glu	Glu	Leu	305	310	315	320
Ser	Cys	Ile	Gly	Glu	Leu	Lys	Lys	Met	Gly	Lys	Ile	Val	Ser	Trp	Cys	325	330	335	
Ser	Gln	Leu	Glu	Val	Leu	Ala	His	Pro	Ala	Leu	Gly	Cys	Phe	Val	Thr	340	345	350	
His	Cys	Gly	Trp	Asn	Ser	Ala	Val	Glu	Ser	Leu	Ser	Cys	Gly	Val	Pro	355	360	365	
Val	Val	Ala	Val	Pro	Gln	Trp	Phe	Asp	Gln	Thr	Thr	Asn	Ala	Lys	Leu	370	375	380	
Ile	Glu	Asp	Ala	Trp	Gly	Thr	Gly	Val	Arg	Val	Arg	Met	Asn	Glu	Gly	385	390	395	400
Gly	Gly	Val	Asp	Gly	Ser	Glu	Ile	Glu	Arg	Cys	Val	Glu	Met	Val	Met	405	410	415	

Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu Asn Ala Ile Lys Trp  
                   420                          425                          430  
 Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp Gly Ser Ser Leu Lys  
                   435                          440                          445  
 Asn Leu Asn Ala Phe Leu His Gln Val Ala Arg Ala  
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                   20                          25                          30  
 Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn  
                   35                          40                          45  
 Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala  
                   50                          55                          60  
 Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Gly Gly Asp Gly Lys  
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 Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn  
                   85                          90                          95  
 Leu Leu Leu Asn Asn Asp Asp Val Thr Phe Val Val Tyr Ser His Leu  
                   100                          105                          110  
 Phe Ala Trp Ala Ala Glu Val Ala Arg Leu Ser His Val Pro Thr Ala  
                   115                          120                          125  
 Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr His Phe Tyr  
                   130                          135                          140  
 Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly Ser Asn Glu Ile Gln  
   145                          150                          155                          160  
 Leu Pro Arg Leu Pro Ser Leu Glu Gln Arg Ser Leu Pro Thr Phe Leu  
                   165                          170                          175  
 Leu Pro Ala Thr Pro Glu Arg Phe Arg Leu Met Met Lys Glu Lys Leu  
                   180                          185                          190

Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val Leu Val Asn Thr Phe  
 195 200 205  
 Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile Asp Arg Tyr Glu Leu  
 210 215 220  
 Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu Asp Gly Glu Asp  
 225 230 235 240  
 Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe Glu Lys Ser Glu Glu  
 245 250 255  
 Asn Asn Cys Val Glu Trp Leu Asn Ser Lys Pro Lys Ser Ser Val Val  
 260 265 270  
 Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro Lys Ala Gln Met Glu  
 275 280 285  
 Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg Pro Phe Leu Trp Met  
 290 295 300  
 Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu Glu Glu Glu Glu  
 305 310 315 320  
 Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys Ile Val Ser  
 325 330 335  
 Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu Gly Cys Phe  
 340 345 350  
 Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu Ser Cys Gly  
 355 360 365  
 Ile Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr Thr Asn Ala  
 370 375 380  
 Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val Arg Met Asn  
 385 390 395 400  
 Glu Gly Gly Gly Val Asp Gly Cys Glu Ile Glu Arg Cys Val Glu Met  
 405 410 415  
 Val Met Asp Gly Gly Asp Lys Thr Lys Leu Val Arg Glu Asn Ala Ile  
 420 425 430  
 Lys Trp Lys Thr Leu Ala Arg Gln Ala Met Gly  
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 <213> Verbena hybrida  
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Ile	Asn	Pro	Ala	Leu	Gln	Phe	Ala	Lys	Arg	Leu	Ala	Asn	Ala	Asp	Ile
			20					25					30		
Gln	Val	Thr	Phe	Phe	Thr	Ser	Val	Tyr	Ala	Trp	Arg	Arg	Met	Ser	Arg
		35					40					45			
Thr	Ala	Ala	Gly	Ser	Asn	Gly	Leu	Ile	Asn	Phe	Val	Ser	Phe	Ser	Asp
	50					55					60				
Gly	Tyr	Asp	Asp	Gly	Leu	Gln	Pro	Gly	Asp	Asp	Gly	Lys	Asn	Tyr	Met
65					70				75						80
Ser	Glu	Met	Lys	Ser	Arg	Gly	Ile	Lys	Ala	Leu	Ser	Asp	Thr	Leu	Ala
			85					90						95	
Ala	Asn	Asn	Val	Asp	Gln	Lys	Ser	Ser	Lys	Ile	Thr	Phe	Val	Val	Tyr
			100					105					110		
Ser	His	Leu	Phe	Ala	Trp	Ala	Ala	Lys	Val	Ala	Arg	Glu	Phe	His	Leu
		115					120					125			
Arg	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala	Thr	Val	Leu	Asp	Ile	Phe
	130					135					140				
Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ser	Asp	Glu	Ile	Asp	Ala	Gly	Ser	Asp
145					150				155						160
Ala	Ile	His	Leu	Pro	Gly	Gly	Leu	Pro	Val	Leu	Ala	Gln	Arg	Asp	Leu
			165					170						175	
Pro	Ser	Phe	Leu	Leu	Pro	Ser	Thr	His	Glu	Arg	Phe	Arg	Ser	Leu	Met
		180						185					190		
Lys	Glu	Lys	Leu	Glu	Thr	Leu	Glu	Gly	Glu	Glu	Lys	Pro	Lys	Val	Leu
		195					200					205			
Val	Asn	Ser	Phe	Asp	Ala	Leu	Glu	Pro	Asp	Ala	Leu	Lys	Ala	Ile	Asp
	210					215					220				
Lys	Tyr	Glu	Met	Ile	Ala	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu
225					230				235						240
Asp	Gly	Lys	Asp	Pro	Ser	Asp	Arg	Ser	Phe	Gly	Gly	Asp	Leu	Phe	Glu
			245					250						255	
Lys	Gly	Ser	Asn	Asp	Asp	Asp	Cys	Leu	Glu	Trp	Leu	Ser	Thr	Asn	Pro
		260					265						270		

Arg Ser Ser Val Val Tyr Val Ser Phe Gly Ser Phe Val Asn Thr Thr  
 275 280 285  
 Lys Ser Gln Met Glu Glu Ile Ala Arg Gly Leu Leu Asp Cys Gly Arg  
 290 295 300  
 Pro Phe Leu Trp Val Val Arg Val Asn Glu Gly Glu Glu Val Leu Ile  
 305 310 315 320  
 Ser Cys Met Glu Glu Leu Lys Arg Val Gly Lys Ile Val Ser Trp Cys  
 325 330 335  
 Ser Gln Leu Glu Val Leu Thr His Pro Ser Leu Gly Cys Phe Val Thr  
 340 345 350  
 His Cys Gly Trp Asn Ser Thr Leu Glu Ser Ile Ser Phe Gly Val Pro  
 355 360 365  
 Met Val Ala Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Leu  
 370 375 380  
 Met Glu Asp Val Trp Arg Thr Gly Val Arg Val Arg Ala Asn Glu Glu  
 385 390 395 400  
 Gly Ser Val Val Asp Gly Asp Glu Ile Arg Arg Cys Ile Glu Glu Val  
 405 410 415  
 Met Asp Gly Gly Glu Lys Ser Arg Lys Leu Arg Glu Ser Ala Gly Lys  
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 Trp Lys Asp Leu Ala Arg Lys Ala Met Glu Glu Asp Gly Ser Ser Val  
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 Asn Asn Leu Lys Val Phe Leu Asp Glu Val Val Gly Ile  
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 <223> Xaa (64) is Cys or Phe, Xaa (65) is Ser or Pro.  
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 Met Val Asn Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly  
 1 5 10 15

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			20						25					30				
Tyr	Val	Asp	Gln	Val	Thr	Phe	Phe	Thr	Ser	Val	Tyr	Ala	Leu	Arg	Arg			
		35						40					45					
Met	Arg	Phe	Glu	Thr	Asp	Pro	Ser	Ser	Arg	Ile	Asp	Phe	Val	Ala	Xaa			
		50					55				60							
Xaa	Asp	Ser	Tyr	Asp	Asp	Gly	Leu	Lys	Lys	Gly	Asp	Asp	Gly	Lys	Asn			
	65				70					75					80			
Tyr	Met	Ser	Glu	Met	Arg	Lys	Arg	Gly	Thr	Lys	Ala	Leu	Lys	Asp	Thr			
				85					90					95				
Leu	Ile	Lys	Leu	Asn	Asp	Ala	Ala	Met	Gly	Ser	Glu	Cys	Tyr	Asn	Arg			
			100					105						110				
Val	Ser	Phe	Val	Val	Tyr	Ser	His	Leu	Phe	Ser	Trp	Ala	Ala	Glu	Val			
		115					120						125					
Ala	Arg	Glu	Val	Asp	Val	Pro	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala			
		130					135					140						
Thr	Val	Phe	Asp	Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp			
	145				150					155					160			
Ile	Asp	Ala	Gly	Ser	Asp	Gln	Ile	Gln	Leu	Pro	Asn	Leu	Pro	Gln	Leu			
			165					170						175				
Ser	Lys	Gln	Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg			
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Phe	Arg	Thr	Leu	Met	Lys	Glu	Lys	Phe	Asp	Thr	Leu	Asp	Lys	Glu	Pro			
		195					200					205						
Lys	Ala	Lys	Val	Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Thr	Glu	Gln			
	210					215					220							
Leu	Lys	Ala	Ile	Asp	Arg	Tyr	Glu	Leu	Ile	Ser	Ile	Gly	Pro	Leu	Ile			
	225				230					235				240				
Pro	Ser	Ser	Ile	Phe	Ser	Asp	Gly	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys			
			245						250					255				
Ser	Tyr	Gly	Gly	Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp			
		260						265					270					
Trp	Leu	Asn	Ser	Lys	Pro	Glu	Ser	Ser	Val	Val	Tyr	Val	Ser	Phe	Gly			
		275						280						285				

Ser Leu Leu Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly  
 290 295 300  
 Leu Ser Asp Thr Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu  
 305 310 315 320  
 Glu Gly Asp Glu Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser  
 325 330 335  
 Phe Phe Asp Arg His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp  
 340 345 350  
 Cys Ser Gln Leu Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val  
 355 360 365  
 Thr His Cys Gly Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val  
 370 375 380  
 Pro Val Val Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys  
 385 390 395 400  
 Met Ile Glu Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu  
 405 410 415  
 Glu Gly Gly Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu  
 420 425 430  
 Val Ile Lys Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly  
 435 440 445  
 Leu Ala Lys Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn  
 450 455 460  
 Leu Lys Asn Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser  
 465 470 475 478

<210> 11

<211> 335

<212> PRT

<213> *Perilla frutescens*

<400> 11

Met Ser Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg  
 1 5 10 15  
 Arg Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu  
 20 25 30  
 Ala Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala  
 35 40 45

Pro Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr  
 50 55 60  
 Gly Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr  
 65 70 75 80  
 Trp Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val  
 85 90 95  
 Asn Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp  
 100 105 110  
 Cys Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly  
 115 120 125  
 Thr Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly  
 130 135 140  
 Gly Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly  
 145 150 155 160  
 Ser Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu  
 165 170 175  
 Phe Thr Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp  
 180 185 190  
 Arg Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser  
 195 200 205  
 Ala Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln  
 210 215 220  
 Trp Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser  
 225 230 235 240  
 Phe Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala  
 245 250 255  
 Ala Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala  
 260 265 270  
 Ile Arg Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu  
 275 280 285  
 Ala Phe Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu  
 290 295 300  
 Lys Asp Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His  
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 Glu Tyr Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro  
 325 330 335  
 <210> 12  
 <211> 468

<212> PRT

<213> Petunia hybrida

<400> 12

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Ile Asn Pro Ala Leu Gln Phe Ala Lys Asn Leu Val Lys Met Gly Ile  
20 25 30  
Glu Val Thr Phe Ser Thr Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu  
35 40 45  
Lys Ser Ile Leu Asn Ala Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser  
50 55 60  
Asp Gly Phe Asp Glu Gly Phe Asp His Ser Lys Asp Pro Val Phe Tyr  
65 70 75 80  
Met Ser Gln Leu Arg Lys Cys Gly Ser Glu Thr Val Lys Lys Ile Ile  
85 90 95  
Leu Thr Cys Ser Glu Asn Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser  
100 105 110  
Ile Phe Leu Pro Trp Ala Ala Glu Val Ala Arg Glu Val His Ile Pro  
115 120 125  
Ser Ala Leu Leu Trp Ser Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr  
130 135 140  
Phe Asn Phe His Gly Tyr Glu Lys Ala Met Ala Asn Glu Ser Asn Asp  
145 150 155 160  
Pro Asn Trp Ser Ile Gln Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg  
165 170 175  
Asp Leu Pro Ser Phe Leu Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg  
180 185 190  
Val Ala Leu Pro Pro Phe Lys Glu Leu Ile Asp Thr Leu Asp Ala Glu  
195 200 205  
Thr Thr Pro Lys Ile Leu Val Asn Thr Phe Asp Glu Leu Glu Pro Glu  
210 215 220  
Ala Leu Asn Ala Ile Glu Gly Tyr Lys Phe Tyr Gly Ile Gly Pro Leu  
225 230 235 240  
Ile Pro Ser Ala Phe Leu Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe  
245 250 255  
Gly Gly Asp Leu Phe Gln Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn  
260 265 270

Ser Lys Pro Asn Ser Ser Val Val Tyr Ile Ser Phe Gly Ser Leu Met  
 275 280 285  
 Asn Pro Ser Ile Ser Gln Met Glu Glu Ile Ser Lys Gly Leu Ile Asp  
 290 295 300  
 Ile Gly Arg Pro Phe Leu Trp Val Ile Lys Glu Asn Glu Lys Gly Lys  
 305 310 315 320  
 Glu Glu Glu Asn Lys Lys Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile  
 325 330 335  
 Gly Lys Ile Val Pro Trp Cys Ser Gln Leu Glu Val Leu Lys His Pro  
 340 345 350  
 Ser Leu Gly Cys Phe Val Ser His Cys Gly Trp Asn Ser Ala Leu Glu  
 355 360 365  
 Ser Leu Ala Cys Gly Val Pro Val Val Ala Phe Pro Gln Trp Thr Asp  
 370 375 380  
 Gln Met Thr Asn Ala Lys Gln Val Glu Asp Val Trp Lys Ser Gly Val  
 385 390 395 400  
 Arg Val Arg Ile Asn Glu Asp Gly Val Val Glu Ser Glu Glu Ile Lys  
 405 410 415  
 Arg Cys Ile Glu Leu Val Met Asp Gly Gly Glu Lys Gly Glu Glu Leu  
 420 425 430  
 Arg Lys Asn Ala Lys Lys Trp Lys Glu Leu Ala Arg Glu Ala Val Lys  
 435 440 445  
 Glu Gly Gly Ser Ser His Lys Asn Leu Lys Ala Phe Ile Asp Asp Val  
 450 455 460  
 Ala Lys Gly Phe  
 465 468

# Sequence

Sequence ID No.: 1

Sequence length: 1507

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Perilla (Perilla frutescens)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p3R4

Sequence:

GAAAAATTC	ACAAAA	ATG	GTC	CGC	CGC	CGC	GTG	CTG	CTA	GCA	ACG	TTT	49
Met Val Arg Arg Arg Val Leu Leu Ala Thr Phe													
1			5			10							
CCT	GCG	CAA	GGC	CAC	ATA	AAT	CCC	GCC	CTC	CAA	TTC	GCC	97
Pro	Ala	Gln	Gly	His	Ile	Asn	Pro	Ala	Leu	Gln	Phe	Ala	
15			20			25							
CTA	AAA	GCC	GGC	ACT	GAC	GTC	ACA	TTT	TTC	ACG	AGC	GTT	145
Leu	Lys	Ala	Gly	Thr	Asp	Val	Thr	Phe	Phe	Thr	Ser	Val	
30			35			40							
CGC	CGC	ATG	GCC	AAC	ACA	GCC	TCC	GCC	GCT	GCC	GGA	AAC	193
Arg	Arg	Met	Ala	Asn	Thr	Ala	Ser	Ala	Ala	Ala	Gly	Asn	
45			50			55							
CTC	GAC	TTC	GTG	GCG	TTC	TCC	GAC	GGC	TAC	GAC	GAC	GGG	241
Leu	Asp	Phe	Val	Ala	Phe	Ser	Asp	Gly	Tyr	Asp	Asp	Gly	
60			65			70			75				
TGC	GGC	GAC	GGG	AAG	CGC	TAC	ATG	TCC	GAG	ATG	AAA	GCC	289
Cys	Gly	Asp	Gly	Lys	Arg	Tyr	Met	Ser	Glu	Met	Lys	Ala	
80			85			90							
GAG	GCC	TTA	AGA	AAC	CTC	CTT	CTC	AAC	AAC	CAC	GAC	GTC	337
Glu	Ala	Leu	Arg	Asn	Leu	Leu	Leu	Asn	Asn	His	Asp	Val	
95			100			105							

GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG CGT GAG TCC	385
Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser	
110 115 120	
CAG GTC CCG AGC GCC CTT CTC TGG GTC GAG CCC GCC ACC GTG CTG TGC	433
Gln Val Pro Ser Ala Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys	
125 130 135	
ATA TAT TAC TTC TAC TTC AAC GGC TAC GCA GAC GAG ATC GAC GCC GGT	481
Ile Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly	
140 145 150 155	
TCC GAC GAA ATT CAG CTC CCT CGG CTT CCA CCC CTG GAG CAG CGC AGT	529
Ser Asp Glu Ile Gln Leu Pro Arg Leu Pro Pro Leu Glu Gln Arg Ser	
160 165 170	
CTT CCG ACC TTT CTG CTG CCG GAG ACA CCG GAG AGA TTC CGG TTG ATG	577
Leu Pro Thr Phe Leu Leu Pro Glu Thr Pro Glu Arg Phe Arg Leu Met	
175 180 185	
ATG AAG GAG AAG CTG GAA ACT TTA GAC GGT GAA GAG AAG GCG AAA GTG	625
Met Lys Glu Lys Leu Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val	
190 195 200	
TTG GTG AAC ACG TTT GAT GCG TTG GAG CCC GAT GCA CTC ACG GCT ATT	673
Leu Val Asn Thr Phe Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile	
205 210 215	
GAT AGG TAT GAG TTG ATC GGG ATC GGG CCG TTG ATT CCC TCC GCC TTC	721
Asp Arg Tyr Glu Leu Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe	
220 225 230 235	
TTG GAC GGC GGA GAT CCC TCC GAA ACG TCT TAC GGC GGC GAT CTT TTC	769
Leu Asp Gly Gly Asp Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe	
240 245 250	
GAA AAA TCG GAG GAG AAT AAC TGC GTG GAG TGG TTG GAC ACG AAG CCG	817
Glu Lys Ser Glu Glu Asn Asn Cys Val Glu Trp Leu Asp Thr Lys Pro	
255 260 265	
AAA TCT TCG GTG GTG TAT GTG TCG TTT GGG AGC GTT TTG AGG TTT CCA	865
Lys Ser Ser Val Val Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro	
270 275 280	
AAG GCA CAA ATG GAA GAG ATT GGG AAA GGG CTA TTA GCC TGC GGA AGG	913
Lys Ala Gln Met Glu Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg	
285 290 295	

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CCG TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC GGC GAA GAA      961
Pro Phe Leu Trp Met Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu
300                      305                      310                      315
GAA GAA GAA GAG TTG AGT TGC ATT GGG GAA TTG AAA AAA ATG GGG AAA      1009
Glu Glu Glu Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys
                      320                      325                      330
ATA GTT TCG TGG TGC TCG CAG TTG GAG GTT CTG GCG CAC CCT GCG TTG      1057
Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu
                      335                      340                      345
GGA TGT TTC GTG ACG CAT TGT GGG TGG AAC TCG GCT GTG GAG AGC TTG      1105
Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu
                      350                      355                      360
AGT TGC GGG GTT CCG GTG GTG GCG GTG CCG CAG TGG TTT GAT CAG ACG      1153
Ser Cys Gly Val Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr
                      365                      370                      375
ACG AAT GCG AAG CTG ATT GAG GAT GCG TGG GGG ACA GGG GTG AGA GTG      1201
Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val
380                      385                      390                      395
AGA ATG AAT GAA GGG GGT GGG GTT GAT GGA TCT GAG ATA GAG AGG TGT      1249
Arg Met Asn Glu Gly Gly Gly Val Asp Gly Ser Glu Ile Glu Arg Cys
                      400                      405                      410
GTG GAG ATG GTG ATG GAT GGG GGT GAG AAG AGC AAA CTA GTG AGA GAA      1297
Val Glu Met Val Met Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu
                      415                      420                      425
AAT GCC ATA AAA TGG AAG ACT TTG GCC AGA GAA GCC ATG GGA GAG GAT      1345
Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp
                      430                      435                      440
GGA TCT TCA CTC AAG AAT CTC AAC GCC TTT CTT CAT CAA GTT GCA CGT      1393
Gly Ser Ser Leu Lys Asn Leu Asn Ala Phe Leu His Gln Val Ala Arg
                      445                      450                      455
GCT TAATACACAA AATGGCTTTC CACTTTTAAT CTACTCAAAC ACCGGTTCAA      1446
Ala
460                                                                1507
ATAAATATCC CCTTCCACTT CTTTCTATTT CACTATCACA TTTATAATTT TAGTAACAAA 1506
A

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Sequence ID No.: 2  
Sequence length: 1470

CCG TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC GGC GAA GAA

Sequence type: Nucleic acid  
Number of strands: Double-strand  
Topology: Straight chain  
Source:

Biological name: Perilla (Perilla frutescens)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p3R6

Sequence:

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ACCAAACCAA AACAAAATTT CCACAAAA ATG GTC CGC CGC CGC GTG CTG CTA      48
                               Met Val Arg Arg Arg Val Leu Leu
                               1           5

GCA ACG TTT CCG GCG CAA GGC CAC ATA AAT CCC GCC CTC CAA TTC GCC      96
Ala Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala
    10           15           20

AAG AGA CTC CTA AAA GCC GGC ACT GAC GTC ACG TTT TTC ACG AGC GTT      144
Lys Arg Leu Leu Lys Ala Gly Thr Asp Val Thr Phe Phe Thr Ser Val
    25           30           35           40

TAT GCA TGG CGC CGC ATG GCC AAC ACA GCC TCC GCC GCT GCC GGA AAC      192
Tyr Ala Trp Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Ala Gly Asn
           45           50           55

CCA CCG GGC CTC GAC TTC GTG GCG TTC TCC GAC GGC TAC GAC GAC GGG      240
Pro Pro Gly Leu Asp Phe Val Ala Phe Ser Asp Gly Tyr Asp Asp Gly
           60           65           70

CTG AAG CCC GGC GGC GAC GGG AAG CGC TAC ATG TCC GAG ATG AAA GCC      288
Leu Lys Pro Gly Gly Asp Gly Lys Arg Tyr Met Ser Glu Met Lys Ala
           75           80           85

CGC GGC TCC GAG GCC TTA AGA AAC CTC CTT CTC AAC AAC GAC GAC GTC      336
Arg Gly Ser Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn Asp Asp Val
           90           95           100

ACT TTC GTC GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG      384
Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala
    105           110           115           120
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094055-0564160

CGT TTG TCC CAC GTC CCG ACC GCC CTT CTC TGG GTC GAG CCC GCC ACC	432
Arg Leu Ser His Val Pro Thr Ala Leu Leu Trp Val Glu Pro Ala Thr	
125 130 135	
GTG CTG TGC ATA TAC CAC TTC TAC TTC AAC GGC TAC GCA GAC GAG ATC	480
Val Leu Cys Ile Tyr His Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile	
140 145 150	
GAC GCC GGT TCC AAT GAA ATT CAG CTC CCT CGG CTT CCA TCC CTG GAG	528
Asp Ala Gly Ser Asn Glu Ile Gln Leu Pro Arg Leu Pro Ser Leu Glu	
155 160 165	
CAG CGC AGT CTT CCG ACG TTT CTG CTG CCT GCG ACG CCG GAG AGA TTC	576
Gln Arg Ser Leu Pro Thr Phe Leu Leu Pro Ala Thr Pro Glu Arg Phe	
170 175 180	
CGG TTG ATG ATG AAG GAG AAG CTG GAA ACT TTA GAC GGT GAA GAG AAG	624
Arg Leu Met Met Lys Glu Lys Leu Glu Thr Leu Asp Gly Glu Glu Lys	
185 190 195 200	
GCG AAA GTA TTG GTG AAC ACG TTT GAT GCG TTG GAG CCC GAT GCA CTC	672
Ala Lys Val Leu Val Asn Thr Phe Asp Ala Leu Glu Pro Asp Ala Leu	
205 210 215	
ACG GCT ATT GAT AGG TAT GAG TTG ATC GGG ATC GGG CCG TTG ATT CCC	720
Thr Ala Ile Asp Arg Tyr Glu Leu Ile Gly Ile Gly Pro Leu Ile Pro	
220 225 230	
TCC GCC TTC TTG GAC GGC GAA GAT CCC TCC GAA ACG TCT TAC GGC GGC	768
Ser Ala Phe Leu Asp Gly Glu Asp Pro Ser Glu Thr Ser Tyr Gly Gly	
235 240 245	
GAT CTT TTC GAA AAA TCG GAG GAG AAT AAC TGC GTG GAG TGG TTG AAC	816
Asp Leu Phe Glu Lys Ser Glu Glu Asn Asn Cys Val Glu Trp Leu Asn	
250 255 260	
TCG AAG CCG AAA TCT TCG GTG GTG TAT GTG TCG TTT GGG AGC GTT TTG	864
Ser Lys Pro Lys Ser Ser Val Val Tyr Val Ser Phe Gly Ser Val Leu	
265 270 275 280	
AGG TTT CCA AAG GCA CAA ATG GAA GAG ATT GGG AAA GGG CTA TTA GCC	912
Arg Phe Pro Lys Ala Gln Met Glu Glu Ile Gly Lys Gly Leu Leu Ala	
285 290 295	
TGC GGA AGG CCC TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC	960
Cys Gly Arg Pro Phe Leu Trp Met Ile Arg Glu Gln Lys Asn Asp Asp	
300 305 310	

004455-0000

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GGC GAA GAA GAA GAA GAA GAA GAA GAG TTG AGT TGC ATT GGG GAA TTG      1008
Gly Glu Glu Glu Glu Glu Glu Glu Glu Leu Ser Cys Ile Gly Glu Leu
      315                      320                      325

AAA AAA ATG GGG AAA ATA GTG TCG TGG TGC TCG CAG TTG GAG GTT CTG      1056
Lys Lys Met Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu
      330                      335                      340

GCG CAC CCT GCG TTG GGA TGT TTC GTG ACG CAT TGT GGG TGG AAC TCG      1104
Ala His Pro Ala Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser
      345                      350                      355                      360

GCT GTG GAG AGC TTG AGT TGC GGG ATT CCG GTG GTG GCG GTG CCG CAG      1152
Ala Val Glu Ser Leu Ser Cys Gly Ile Pro Val Val Ala Val Pro Gln
      365                      370                      375

TGG TTT GAT CAG ACG ACG AAT GCG AAG CTG ATT GAG GAT GCG TGG GGG      1200
Trp Phe Asp Gln Thr Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly
      380                      385                      390

ACA GGG GTG AGA GTG AGA ATG AAT GAA GGG GGT GGG GTT GAT GGA TGT      1248
Thr Gly Val Arg Val Arg Met Asn Glu Gly Gly Gly Val Asp Gly Cys
      395                      400                      405

GAG ATA GAA AGG TGT GTG GAG ATG GTG ATG GAT GGG GGT GAC AAG ACC      1296
Glu Ile Glu Arg Cys Val Glu Met Val Met Asp Gly Gly Asp Lys Thr
      410                      415                      420

AAA CTA GTG AGA GAA AAT GCC ATC AAA TGG AAG ACT TTG GCC AGA CAA      1344
Lys Leu Val Arg Glu Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Gln
      425                      430                      435                      440

GCC ATG GGA TAGGATGGAT CTTCACTCAA CAATCTCAAC GCCTTTCTTC      1393
Ala Met Gly
      443

GTCAAGTTGC ACACTTTTAA TCTGCTCAAA CAGCGGTTCA AATAAATATC CCCTTCCACT 1453
TAAAAAAAAA AAAAAAA
                                         1470

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Sequence ID No.: 3

Sequence length: 2062

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Verbena (Verbena hybrida)

Tissue type: Petal

Direct source:

Library name: cDNA library

Clone name: pSHGT8

Sequence:

ATTTTACCAA AAAAATAAAAA AAAAA ATG AGC AGA GCT CAC GTC CTC TTG GCC	52
Met Ser Arg Ala His Val Leu Leu Ala	
1 5	
ACA TTC CCA GCA CAG GGA CAC ATA AAT CCC GCC CTT CAA TTC GCC AAG	100
Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala Lys	
10 15 20 25	
CGT CTC GCA AAT GCC GAC ATT CAA GTC ACA TTC TTC ACC AGC GTC TAC	148
Arg Leu Ala Asn Ala Asp Ile Gln Val Thr Phe Phe Thr Ser Val Tyr	
30 35 40	
GCA TGG CGC CGC ATG TCC AGA ACC GCC GCT GGC TCA AAC GGG CTC ATC	196
Ala Trp Arg Arg Met Ser Arg Thr Ala Ala Gly Ser Asn Gly Leu Ile	
45 50 55	
AAT TTT GTG TCG TTT TCC GAC GGG TAT GAC GAC GGG TTA CAG CCC GGA	244
Asn Phe Val Ser Phe Ser Asp Gly Tyr Asp Asp Gly Leu Gln Pro Gly	
60 65 70	
GAC GAT GGG AAG AAC TAC ATG TCG GAG ATG AAA AGC AGA GGT ATA AAA	292
Asp Asp Gly Lys Asn Tyr Met Ser Glu Met Lys Ser Arg Gly Ile Lys	
75 80 85	
GCC TTG AGC GAT ACT CTT GCA GCC AAT AAT GTC GAT CAA AAA AGC AGC	340
Ala Leu Ser Asp Thr Leu Ala Ala Asn Asn Val Asp Gln Lys Ser Ser	
90 95 100 105	
AAA ATC ACG TTC GTG GTG TAC TCC CAC CTC TTT GCA TGG GCG GCC AAG	388
Lys Ile Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Lys	
110 115 120	
GTG GCG CGT GAG TTC CAT CTC CGG AGC GCG CTA CTC TGG ATT GAG CCA	436
Val Ala Arg Glu Phe His Leu Arg Ser Ala Leu Leu Trp Ile Glu Pro	
125 130 135	
GCT ACG GTG TTG GAT ATA TTT TAC TTT TAT TTC AAC GGC TAT AGC GAC	484
Ala Thr Val Leu Asp Ile Phe Tyr Phe Tyr Phe Asn Gly Tyr Ser Asp	
140 145 150	

564260" 5354460

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Glu Ile Asp Ala Gly Ser Asp Ala Ile His Leu Pro Gly Gly Leu Pro	
155 160 165	
GTG CTG GCC CAG CGT GAT TTA CCG TCT TTC CTT CTT CCT TCC ACG CAT	580
Val Leu Ala Gln Arg Asp Leu Pro Ser Phe Leu Leu Pro Ser Thr His	
170 175 180 185	
GAG AGA TTC CGT TCA CTG ATG AAG GAG AAA TTG GAA ACT TTA GAA GGT	628
Glu Arg Phe Arg Ser Leu Met Lys Glu Lys Leu Glu Thr Leu Glu Gly	
190 195 200	
GAA GAA AAA CCT AAG GTC TTG GTG AAC AGC TTT GAT GCG TTG GAG CCT	676
Glu Glu Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu Glu Pro	
205 210 215	
GAT GCG CTC AAG GCC ATT GAT AAG TAC GAG ATG ATT GCA ATC GGG CCG	724
Asp Ala Leu Lys Ala Ile Asp Lys Tyr Glu Met Ile Ala Ile Gly Pro	
220 225 230	
TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAC AGG TCT	772
Leu Ile Pro Ser Ala Phe Leu Asp Gly Lys Asp Pro Ser Asp Arg Ser	
235 240 245	
TTC GGC GGA GAT TTG TTC GAG AAA GGG TCG AAT GAC GAC GAT TGC CTC	820
Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asn Asp Asp Asp Cys Leu	
250 255 260 265	
GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC	868
Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe	
270 275 280	
GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA	916
Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg	
285 290 295	
GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC	964
Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn	
300 305 310	
GAA GGA GAA GAG GTA TTG ATA AGT TGC ATG GAG GAG TTG AAA CGA GTG	1012
Glu Gly Glu Glu Val Leu Ile Ser Cys Met Glu Glu Leu Lys Arg Val	
315 320 325	
GGG AAA ATT GTA TCT TGG TGT TCT CAA TTG GAA GTC CTG ACG CAT CCC	1060
Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Thr His Pro	
330 335 340 345	

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TCG TTG GGA TGT TTC GTG ACA CAC TGC GGG TGG AAT TCG ACT CTA GAG      1108
Ser Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
          350                      355                      360
AGT ATA TCT TTC GGG GTT CCG ATG GTG GCT TTT CCG CAG TGG TTC GAT      1156
Ser Ile Ser Phe Gly Val Pro Met Val Ala Phe Pro Gln Trp Phe Asp
          365                      370                      375
CAA GGG ACG AAT GCG AAG CTG ATG GAG GAT GTG TGG AGG ACG GGT GTG      1204
Gln Gly Thr Asn Ala Lys Leu Met Glu Asp Val Trp Arg Thr Gly Val
          380                      385                      390
AGA GTG AGA GCT AAT GAG GAG GGT AGC GTC GTT GAT GGT GAT GAA ATT      1252
Arg Val Arg Ala Asn Glu Glu Gly Ser Val Val Asp Gly Asp Glu Ile
          395                      400                      405
AGG AGA TGT ATT GAG GAG GTT ATG GAT GGG GGA GAA AAG AGT AGG AAA      1300
Arg Arg Cys Ile Glu Glu Val Met Asp Gly Gly Glu Lys Ser Arg Lys
          410                      415                      420                      425
CTT AGA GAG AGT GCT GGC AAG TGG AAG GAT TTG GCA AGA AAA GCT ATG      1348
Leu Arg Glu Ser Ala Gly Lys Trp Lys Asp Leu Ala Arg Lys Ala Met
          430                      435                      440
GAG GAA GAT GGA TCT TCA GTT AAC AAC CTC AAG GTC TTT CTT GAT GAG      1396
Glu Glu Asp Gly Ser Ser Val Asn Asn Leu Lys Val Phe Leu Asp Glu
          445                      450                      455
GTT GTA GGT ATC TAAAGACGTA AATGAGGTCC CCATAGGCAA AATTGCAAAT      1448
Val Val Gly Ile
          460 461
TTCATCTCGT AAGTTGAATA CTTTTTGGCT TTAATTTTGT TCGAGTTTGT TTTTCAAAAT      1508
TTATCTTGTA ATTTTACATT GAGTGTAAT TTAGTCTGAT TTAACTGGA AAAATATAAA      1568
ATTCATTGTT GAGACTCTTC ATCAAAATCA TCTGATTTCC TTTATTGTCT TGGTCAAAAT      1628
TCTCATATCA ATTGGAAAAA ATAAATTTCA AAATCGTCCA ATTTTGAACC AAGAAAGAAG      1688
TATAATTTGA CCAAAATAAT AAAAGGATTC AAGTGATCTT GATGAAGTGT CTGAGCGACG      1748
AGTTCTATAT TTTTCCACCG AATTTCTAAC GAGTTTTTGA ATTTTTTTTA GCCAAAATCG      1808
GACTAACTTT GTACAAAATG AAAAGTTATA TGATGAAATT TTAAAAACA AACTCAGACA      1868
ATAATAAAGC CCGAAAGTAG TAAAATTACC TGACGAAATT TGCAATTTCC CCTCCTATTT      1928
TAATTTTTTTT GGTGTGTTA ATAAATCGGT TATTTTACTT TTAATTAAAA TAAAAGTGAG      1988
ATGCATGATA GCTTGGTGAG TATATATGAG TTGATGGTAA TGTACGATAT TTTCTAAAAA      2048
AAAAAAAAAA AAAA
          2062

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Sequence ID No.: 4

Sequence length: 1671

Sequence type: Nucleic acid  
Number of strands: Double-strand  
Topology: Straight chain  
Source:

Biological name: Trenia

Tissue type: Petal

Direct source:

Library name: cDNA library

Clone name: pSTGT5

Sequence:

AACACATAAA AAAAAAATAA AAGAAGAAAT AATTAAAAAA AAAA ATG GTT AAC 53  
Met Val Asn  
1  
AAA CGC CAT ATT CTA CTA GCA ACA TTC CCA GCA CAA GGC CAC ATA AAC 101  
Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn  
5 10 15  
CCT TCT CTC GAG TTC GCC AAA AGG CTC CTC AAC ACC GGA TAC GTC GAC 149  
Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp  
20 25 30 35  
CAA GTC ACA TTC TTC ACG AGT GTA TAC GCA TTG AGA CGC ATG CGC TTC 197  
Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe  
40 45 50  
GAA ACC GAT CCG AGC AGC AGA ATC GAT TTC GTG GCA TKT YCA GAT TCT 245  
Glu Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser  
55 60 65  
TAC GAT GAT GGC TTA AAG AAA GGC GAC GAT GGC AAA AAC TAC ATG TCG 293  
Tyr Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn Tyr Met Ser  
70 75 80  
GAG ATG AGA AAG CGC GGA ACG AAG GCC TTA AAG GAC ACT CTT ATT AAG 341  
Glu Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr Leu Ile Lys  
85 90 95  
CTC AAC GAT GCT GCG ATG GGA AGT GAA TGT TAC AAT CGC GTG AGC TTT 389  
Leu Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg Val Ser Phe  
100 105 110 115

GTG GTG TAC TCT CAT CTA TTT TCG TGG GCA GCT GAA GTG GCG CGT GAA	437
Val Val Tyr Ser His Leu Phe Ser Trp Ala Ala Glu Val Ala Arg Glu	
120 125 130	
GTC GAC GTG CCG AGT GCC CTT CTT TGG ATT GAA CCG GCT ACG GTT TTC	485
Val Asp Val Pro Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Phe	
135 140 145	
GAT GTG TAC TAT TTT TAC TTC AAT GGG TAT GCC GAT GAT ATC GAT GCG	533
Asp Val Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Asp Ile Asp Ala	
150 155 160	
GGC TCA GAT CAA ATC CAA CTG CCC AAT CTT CCG CAG CTC TCC AAG CAA	581
Gly Ser Asp Gln Ile Gln Leu Pro Asn Leu Pro Gln Leu Ser Lys Gln	
165 170 175	
GAT CTC CCC TCT TTC CTA CTC CCT TCG AGC CCC GCG AGA TTC CGA ACC	629
Asp Leu Pro Ser Phe Leu Leu Pro Ser Ser Pro Ala Arg Phe Arg Thr	
180 185 190 195	
CTA ATG AAA GAA AAG TTC GAC ACG CTC GAC AAA GAA CCG AAA GCG AAG	677
Leu Met Lys Glu Lys Phe Asp Thr Leu Asp Lys Glu Pro Lys Ala Lys	
200 205 210	
GTC TTG ATA AAC ACG TTC GAC GCA TTA GAA ACC GAA CAA CTC AAA GCC	725
Val Leu Ile Asn Thr Phe Asp Ala Leu Glu Thr Glu Gln Leu Lys Ala	
215 220 225	
ATC GAC AGG TAT GAA CTA ATA TCC ATC GGC CCA TTA ATC CCA TCA TCG	773
Ile Asp Arg Tyr Glu Leu Ile Ser Ile Gly Pro Leu Ile Pro Ser Ser	
230 235 240	
ATA TTC TCA GAT GGC AAC GAC CCC TCA TCA AGC AAC AAA TCC TAC GGT	821
Ile Phe Ser Asp Gly Asn Asp Pro Ser Ser Ser Asn Lys Ser Tyr Gly	
245 250 255	
GGA GAC CTC TTC AGA AAA GCC GAT GAA ACT TAC ATG GAC TGG CTA AAC	869
Gly Asp Leu Phe Arg Lys Ala Asp Glu Thr Tyr Met Asp Trp Leu Asn	
260 265 270 275	
TCA AAA CCC GAA TCA TCG GTC GTT TAC GTT TCG TTC GGG AGC CTC CTG	917
Ser Lys Pro Glu Ser Ser Val Val Tyr Val Ser Phe Gly Ser Leu Leu	
280 285 290	
AGG CTC CCG AAA CCC CAA ATG GAA GAA ATA GCA ATA GGG CTT TCA GAC	965
Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly Leu Ser Asp	
295 300 305	

ACC	AAA	TCG	CCA	GTT	CTC	TGG	GTG	ATA	AGA	AGA	AAC	GAA	GAG	GGC	GAC	1013
Thr	Lys	Ser	Pro	Val	Leu	Trp	Val	Ile	Arg	Arg	Asn	Glu	Glu	Gly	Asp	
310			315			320										
GAA	CAA	GAG	CAA	GCA	GAA	GAA	GAA	GAG	AAG	CTG	CTG	AGC	TTC	TTT	GAT	1061
Glu	Gln	Glu	Gln	Ala	Glu	Glu	Glu	Glu	Lys	Leu	Leu	Ser	Phe	Phe	Asp	
325			330			335										
CGT	CAC	GGA	ACT	GAA	CGA	CTC	GGG	AAA	ATC	GTG	ACA	TGG	TGC	TCA	CAA	1109
Arg	His	Gly	Thr	Glu	Arg	Leu	Gly	Lys	Ile	Val	Thr	Trp	Cys	Ser	Gln	
340			345			350			355							
TTG	GAT	GTT	CTG	ACG	CAT	AAG	TCG	GTG	GGA	TGC	TTC	GTG	ACG	CAT	TGC	1157
Leu	Asp	Val	Leu	Thr	His	Lys	Ser	Val	Gly	Cys	Phe	Val	Thr	His	Cys	
360			365			370										
GGT	TGG	AAT	TCT	GCT	ATC	GAG	AGC	CTG	GCT	TGT	GGT	GTG	CCC	GTG	GTG	1205
Gly	Trp	Asn	Ser	Ala	Ile	Glu	Ser	Leu	Ala	Cys	Gly	Val	Pro	Val	Val	
375			380			385										
TGC	TTT	CCT	CAA	TGG	TTC	GAT	CAA	GGG	ACT	AAT	GCG	AAG	ATG	ATC	GAA	1253
Cys	Phe	Pro	Gln	Trp	Phe	Asp	Gln	Gly	Thr	Asn	Ala	Lys	Met	Ile	Glu	
390			395			400										
GAT	GTG	TGG	AGG	AGT	GGT	GTG	AGA	GTC	AGA	GTG	AAT	GAG	GAA	GGC	GGC	1301
Asp	Val	Trp	Arg	Ser	Gly	Val	Arg	Val	Arg	Val	Asn	Glu	Glu	Gly	Gly	
405			410			415										
GTT	GTT	GAT	AGG	CGT	GAG	ATT	AAG	AGG	TGC	GTC	TCG	GAG	GTT	ATA	AAG	1349
Val	Val	Asp	Arg	Arg	Glu	Ile	Lys	Arg	Cys	Val	Ser	Glu	Val	Ile	Lys	
420			425			430			435							
AGT	CGA	GAG	TTG	AGA	GAA	AGC	GCA	ATG	ATG	TGG	AAG	GGT	TTG	GCT	AAA	1397
Ser	Arg	Glu	Leu	Arg	Glu	Ser	Ala	Met	Met	Trp	Lys	Gly	Leu	Ala	Lys	
440			445			450										
GAA	GCT	ATG	GAT	GAA	GAA	CGT	GGA	TCA	TCA	ATG	AAC	AAT	CTG	AAG	AAT	1445
Glu	Ala	Met	Asp	Glu	Glu	Arg	Gly	Ser	Ser	Met	Asn	Asn	Leu	Lys	Asn	
455			460			465										
TTT	ATT	ACT	AGG	ATT	ATT	AAT	GAA	AAT	GCC	TCA	TAAGTTGTAC					1488
Phe	Ile	Thr	Arg	Ile	Ile	Asn	Glu	Asn	Ala	Ser						
470			475			478										
TATATATGTT ATTATTGTTG TTATGGACGT CGAATTAAGT ATTAGTTAAA TGATATGTAT																1548
TTAGAGGAAG GCCAAAACGG GCTACACCCG GCAGGCCACG GGTGGGAAAA GCCCGCCATG																1608
ATTTAAAATA TATATTTTAA AATAAATATT TTCTACTATT AAATAAAAA AAAAAAAAAA																1668
AAA																1671

Sequence ID No.: 5  
Sequence length: 1437  
Sequence type: Nucleic acid  
Number of strands: Double-strand  
Topology: Straight chain  
Source:

Biological name: *Perilla* (*Perilla frutescens*)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p8R6

Sequence:

TTCAAACTC ATAACGTGAT TGAGCTAATG TGCACATCTT CCTCTTCAAA GTCTACAGTG 60  
TCATCCTACC AGCATCATCA TGATCAATCT CTTTATAATG AGGAGAATGG AGTAACAAGG 120  
AGTGGGTTTT GTTACTCAGC TTCAACCTAC GTACGTACTA CTACTGACTC AACTCTCAAG 180  
AGAATGAATA TAATATATAA TGGGCGATAG ATCTTTGTAG ATATGTAGGT GTAGCCTGCA 240  
GGTGGTTAAT TAATTTCCGG TGTGGGAAAA TAAATAAATA AATAAATATA GCG ATG AGC 299

Met Ser

1

AGC AGC AGC AGC AGA AGG TGG AGA GAG AAT GAG GGG ATG CGA AGG ACA 347  
Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg Thr

5

10

15

TTG CTG GGG TTG GGT TTG GGG CAG TTG GTT TCT TTC GAT TTG GCT ATC 395  
Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala Ile

20

25

30

ATG ACC TTT TCT GCT TCT TTG GTT TCA ACC ACA GTG GAT GCA CCA CTT 443  
Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro Leu

35

40

45

50

ACT ATG TCG TTC ACT ACA TAC ACT GTT GTG GCC CTG CTC TAT GGA ACC 491  
Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly Thr

55

60

65

ATC TTG CTT TAC CGC CGC CAC AAA TTC TTG GTT CCA TGG TAC TGG TAT 539  
Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr

70

75

80

GCT	CTC	CTG	GGG	TTC	GTG	GAC	GTC	CAC	GGC	AAT	TAT	CTT	GTT	AAT	AAA	587
Ala	Leu	Leu	Gly	Phe	Val	Asp	Val	His	Gly	Asn	Tyr	Leu	Val	Asn	Lys	
85						90						95				
GCA	TTC	GAG	TTG	ACA	TCG	ATT	ACG	AGT	GTG	AGC	ATA	CTG	GAT	TGT	TGG	635
Ala	Phe	Glu	Leu	Thr	Ser	Ile	Thr	Ser	Val	Ser	Ile	Leu	Asp	Cys	Trp	
100						105						110				
ACA	ATC	GTG	TGG	TCC	ATC	ATC	TTT	ACA	TGG	ATG	TTC	CTA	GGC	ACA	AAA	683
Thr	Ile	Val	Trp	Ser	Ile	Ile	Phe	Thr	Trp	Met	Phe	Leu	Gly	Thr	Lys	
115						120						125			130	
TAC	TCT	GTA	TAC	CAG	TTT	GTC	GGT	GCT	GCT	ATT	TGT	GTA	GGA	GGC	CTC	731
Tyr	Ser	Val	Tyr	Gln	Phe	Val	Gly	Ala	Ala	Ile	Cys	Val	Gly	Gly	Leu	
			135						140						145	
CTC	CTC	GTG	CTT	CTT	TCC	GAC	TCA	GGG	GTC	ACT	GCT	GCT	GGT	TCG	AAT	779
Leu	Leu	Val	Leu	Leu	Ser	Asp	Ser	Gly	Val	Thr	Ala	Ala	Gly	Ser	Asn	
			150						155						160	
CCT	CTT	TTG	GGT	GAT	TTT	CTT	GTC	ATA	ACA	GGC	TCT	ATT	TTG	TTC	ACA	827
Pro	Leu	Leu	Gly	Asp	Phe	Leu	Val	Ile	Thr	Gly	Ser	Ile	Leu	Phe	Thr	
165						170						175				
CTC	AGC	ACT	GTT	GGT	CAG	GAA	TAC	TGC	GTG	AAG	AGG	AAA	GAT	CGT	ATT	875
Leu	Ser	Thr	Val	Gly	Gln	Glu	Tyr	Cys	Val	Lys	Arg	Lys	Asp	Arg	Ile	
180						185						190				
GAA	GTA	GTA	GCA	ATG	ATC	GGT	GTA	TTT	GGT	ATG	CTC	ATC	AGT	GCA	ACC	923
Glu	Val	Val	Ala	Met	Ile	Gly	Val	Phe	Gly	Met	Leu	Ile	Ser	Ala	Thr	
195						200						205			210	
GAG	ATT	ACT	GTG	CTG	GAG	AGG	AAT	GCC	CTC	TCA	TCA	ATG	CAG	TGG	TCT	971
Glu	Ile	Thr	Val	Leu	Glu	Arg	Asn	Ala	Leu	Ser	Ser	Met	Gln	Trp	Ser	
			215						220						225	
ACT	GGA	CTT	TTG	GCA	GCC	TAT	GTT	GTT	TAT	GCA	CTG	TCC	AGC	TTC	CTC	1019
Thr	Gly	Leu	Leu	Ala	Ala	Tyr	Val	Val	Tyr	Ala	Leu	Ser	Ser	Phe	Leu	
			230						235						240	
TTC	TGC	ACA	CTC	ACC	CCT	TTT	CTT	CTC	AAG	ATG	AGT	GGC	GCT	GCA	TTT	1067
Phe	Cys	Thr	Leu	Thr	Pro	Phe	Leu	Leu	Lys	Met	Ser	Gly	Ala	Ala	Phe	
245						250						255				
TTC	AAT	CTT	TCC	ATG	CTT	ACA	TCT	GAT	ATG	TGG	GCT	GTT	GCA	ATT	AGG	1115
Phe	Asn	Leu	Ser	Met	Leu	Thr	Ser	Asp	Met	Trp	Ala	Val	Ala	Ile	Arg	
260						265						270				

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ACA TTC ATA TAC AAC CAG GAG GTT GAT TGG TTA TAC TAT TTG GCC TTT      1163
Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala Phe
275                      280                      285                      290
TGT CTC GTT GTT GTT GGA ATA TTC ATA TAT ACA AAA ACA GAG AAG GAT      1211
Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys Asp
                      295                      300                      305
CCT AAC AAT ACG AGA GCC CTT GAG AAT GGA AAC TTG GAT CAT GAA TAT      1259
Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu Tyr
                      310                      315                      320
AGT CTC CTT GAG GAT CAA GAT GAC ACA CCA AGA AAA CCA TAGCTAGCTT      1308
Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro
                      325                      330                      335
TGCCCAACAAT CTTTTCATCA ACAGTTTAA ATAATTCGTG AGGGGGAGAG AGATCGAGAT      1368
ACTAATTAAT GGACGTCTAT TATATAGTTG GAGGTTTTTG TTTTATTAT TTATTGAGT      1428
AAAAAAAAA                                         1437

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Sequence ID No.: 6

Sequence length: 2105

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Petunia

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: pSPGT1

Sequence:

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AGTGAGCGCA ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC      60
TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA      120
AACAGCTATG ACCATGATTA CGCCAAGCTC GAAATTAACC CTCACTAAAG GGAACAAAAG      180
CTGGAGCTCC ACGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG CTGCAGGAAT      240
TCCGTTGCTG TCGCCACAAT TTACAAACCA AGAAATTAAG CATCCCTTTC CCCCCTTAA      300
AAAACATACA AGTTTTTAAT TTTTCACTAA GCAAGAAAAT ATG GTG CAG CCT CAT GTC      358
Met Val Gln Pro His Val

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ATC TTA ACA ACA TTT CCA GCA CAA GGC CAT ATT AAT CCA GCA CTT CAA	406
Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln	
10 15 20	
TTT GCC AAG AAT CTT GTC AAG ATG GGC ATA GAA GTG ACA TTT TCT ACA	454
Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr	
25 30 35	
AGC ATT TAT GCC CAA AGC CGT ATG GAT GAA AAA TCC ATT CTT AAT GCA	502
Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala	
40 45 50	
CCA AAA GGA TTG AAT TTC ATT CCA TTT TCC GAT GGC TTT GAT GAA GGT	550
Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser Asp Gly Phe Asp Glu Gly	
55 60 65 70	
TTT GAT CAT TCA AAA GAC CCT GTA TTT TAC ATG TCA CAA CTT CGT AAA	598
Phe Asp His Ser Lys Asp Pro Val Phe Tyr Met Ser Gln Leu Arg Lys	
75 80 85	
TGT GGA AGT GAA ACT GTC AAA AAA ATA ATT CTC ACT TGC TCT GAA AAT	646
Cys Gly Ser Glu Thr Val Lys Lys Ile Ile Leu Thr Cys Ser Glu Asn	
90 95 100	
GGA CAG CCT ATA ACT TGC CTA CTT TAC TCC ATT TTC CTT CCT TGG GCA	694
Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser Ile Phe Leu Pro Trp Ala	
105 110 115	
GCA GAG GTA GCA CGT GAA GTT CAC ATC CCT TCT GCT CTT CTT TGG AGT	742
Ala Glu Val Ala Arg Glu Val His Ile Pro Ser Ala Leu Leu Trp Ser	
120 125 130	
CAA CCA GCA ACA ATA TTG GAC ATA TAT TAC TTC AAC TTT CAT GGA TAT	790
Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr Phe Asn Phe His Gly Tyr	
135 140 145 150	
GAA AAA GCT ATG GCT AAT GAA TCC AAT GAT CCA AAT TGG TCC ATT CAA	838
Glu Lys Ala Met Ala Asn Glu Ser Asn Asp Pro Asn Trp Ser Ile Gln	
155 160 165	
CTT CCC GGG CTT CCA CTA CTG GAA ACT CGA GAT CTT CCT TCA TTT TTA	886
Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg Asp Leu Pro Ser Phe Leu	
170 175 180	
CTT CCT TAT GGT GCA AAA GGG AGT CTT CGA GTT GCA CTT CCA CCA TTC	934
Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg Val Ala Leu Pro Pro Phe	
185 190 195	

AAA	GAA	TTG	ATA	GAC	ACA	TTA	GAT	GCT	GAA	ACC	ACT	CCT	AAG	ATT	CTT	982
Lys	Glu	Leu	Ile	Asp	Thr	Leu	Asp	Ala	Glu	Thr	Thr	Pro	Lys	Ile	Leu	
200			205			210										
GTG	AAT	ACA	TTT	GAT	GAA	TTA	GAG	CCT	GAG	GCA	CTC	AAT	GCA	ATT	GAA	1030
Val	Asn	Thr	Phe	Asp	Glu	Leu	Glu	Pro	Glu	Ala	Leu	Asn	Ala	Ile	Glu	
215			220			225			230							
GGT	TAT	AAG	TTT	TAT	GGA	ATT	GGA	CCG	TTG	ATT	CCT	TCT	GCT	TTC	TTG	1078
Gly	Tyr	Lys	Phe	Tyr	Gly	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ala	Phe	Leu	
235			240			245										
GGT	GGA	AAT	GAC	CCT	TTA	GAT	GCT	TCA	TTT	GGT	GGT	GAT	CTT	TTT	CAA	1126
Gly	Gly	Asn	Asp	Pro	Leu	Asp	Ala	Ser	Phe	Gly	Gly	Asp	Leu	Phe	Gln	
250			255			260										
AAT	TCA	AAT	GAC	TAT	ATG	GAA	TGG	TTA	AAC	TCA	AAG	CCA	AAT	TCA	TCA	1174
Asn	Ser	Asn	Asp	Tyr	Met	Glu	Trp	Leu	Asn	Ser	Lys	Pro	Asn	Ser	Ser	
265			270			275										
GTT	GTT	TAT	ATA	TCT	TTT	GGG	AGT	CTA	ATG	AAT	CCA	TCT	ATT	AGC	CAA	1222
Val	Val	Tyr	Ile	Ser	Phe	Gly	Ser	Leu	Met	Asn	Pro	Ser	Ile	Ser	Gln	
280			285			290										
ATG	GAG	GAG	ATA	TCA	AAA	GGG	TTG	ATA	GAC	ATA	GGA	AGG	CCG	TTT	TTA	1270
Met	Glu	Glu	Ile	Ser	Lys	Gly	Leu	Ile	Asp	Ile	Gly	Arg	Pro	Phe	Leu	
295			300			305			310							
TGG	GTG	ATA	AAA	GAA	AAT	GAA	AAA	GGC	AAA	GAA	GAA	GAG	AAT	AAA	AAG	1318
Trp	Val	Ile	Lys	Glu	Asn	Glu	Lys	Gly	Lys	Glu	Glu	Glu	Asn	Lys	Lys	
315			320			325										
CTT	GGT	TGT	ATT	GAA	GAA	TTG	GAA	AAA	ATA	GGA	AAA	ATA	GTT	CCA	TGG	1366
Leu	Gly	Cys	Ile	Glu	Glu	Leu	Glu	Lys	Ile	Gly	Lys	Ile	Val	Pro	Trp	
330			335			340										
TGT	TCA	CAA	CTT	GAA	GTT	CTA	AAA	CAT	CCA	TCT	TTA	GGA	TGT	TTT	GTT	1414
Cys	Ser	Gln	Leu	Glu	Val	Leu	Lys	His	Pro	Ser	Leu	Gly	Cys	Phe	Val	
345			350			355										
TCT	CAT	TGT	GGA	TGG	AAT	TCA	GCC	TTA	GAG	AGT	TTA	GCT	TGT	GGA	GTG	1462
Ser	His	Cys	Gly	Trp	Asn	Ser	Ala	Leu	Glu	Ser	Leu	Ala	Cys	Gly	Val	
360			365			370										
CCA	GTT	GTG	GCA	TTT	CCT	CAA	TGG	ACA	GAT	CAA	ATG	ACA	AAT	GCC	AAA	1510
Pro	Val	Val	Ala	Phe	Pro	Gln	Trp	Thr	Asp	Gln	Met	Thr	Asn	Ala	Lys	
375			380			385			390							

CAA GTT GAA GAT GTG TGG AAA AGT GGA GTA AGA GTG AGA ATA AAT GAA 1558  
Gln Val Glu Asp Val Trp Lys Ser Gly Val Arg Val Arg Ile Asn Glu  
395 400 405  
GAT GGT GTT GTT GAA AGT GAG GAA ATC AAA AGG TGT ATT GAA TTG GTA 1606  
Asp Gly Val Val Glu Ser Glu Glu Ile Lys Arg Cys Ile Glu Leu Val  
410 415 420  
ATG GAT GGA GGA GAG AAA GGG GAA GAA TTG AGA AAG AAT GCT AAG AAA 1654  
Met Asp Gly Gly Glu Lys Gly Glu Glu Leu Arg Lys Asn Ala Lys Lys  
425 430 435  
TGG AAA GAA TTG GCT AGA GAA GCT GTG AAG GAA GGT GGA TCT TCA CAC 1702  
Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His  
440 445 450  
AAG AAT TTA AAG GCT TTT ATT GAT GAT GTT GCC AAA GGG TTT TAATATTTAC 1754  
Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe  
455 460 465 468  
AGGCTTTTGC CGTGATATTA CTTCCCCTAG TTGGCGATTC ACTCTTTGTG GACTTGCTTG 1814  
ACAAAAAACT GAGGGAATGT GCTAAGACAC GCTAATGCTT TAAGAAGTCA TTTCCAAGGC 1874  
TTGAAGCCTG CTTTAAAAAC TTATTAGCCA GTAATCTATA GGGTTCTCTT CTATTTTCT 1934  
CTGTCTCTCT TTTTAGCCTT TTTCTTTCCA AGGTTTAAGA ATAGCGTGAA CATAGCTTAG 1994  
TACGTAGTCT TGGTATCTCT ATCTTACCAA GTGCAAGATT ATGCTTATGC TGTCTCCTA 2054  
AATTTCTTAA TAAAATGCAA GATGAAAAAG TACAAAAAAA AAAAAAAAAA A 2105

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